combinatorial library comprising compounds of the general formula XY$_n$ wherein n is an integer from 2 to about 6, X is a scaffold [having n reactive groups], and each Y is, independently, a peripheral moiety, [wherein each reactive group is capable of reacting with at least one peripheral moiety precursor to form a covalent bond, and] wherein said mass-coded combinatorial library is produced by reacting a scaffold precursor having n reactive groups, wherein each reactive group is capable of reacting with at least one peripheral moiety precursor to form a covalent bond, with a peripheral moiety precursor subset selected from a peripheral moiety precursor set, said peripheral moiety precursor subset comprising a sufficient number of distinct peripheral moiety precursors such that there exist at least about 250 distinct combinations of n peripheral moieties derived from said peripheral moiety precursors, [wherein said subset includes at least two different peripheral moiety precursors that are each contacted with and can each react with at least two different reactive groups,] said method comprising the steps of:

(a) contacting the first biomolecule with the mass-coded combinatorial library, whereby members of the mass-coded combinatorial library which are ligands for the biomolecule bind to the first biomolecule to form first biomolecule-ligand complexes and members of the mass-coded library which are not ligands for the first biomolecule remain unbound;

(b) separating the first biomolecule-ligand complexes from the unbound members of the mass-coded combinatorial library;

(c) dissociating the first biomolecule-ligand complexes; and

(d) determining the molecular mass of each ligand to identify the set of n peripheral moieties present in each ligand;

wherein the molecular mass of each ligand corresponds to a set of n peripheral moieties present in that ligand, thereby identifying a member of the mass-coded combinatorial library which is a ligand for the first biomolecule.

52. (*Amended*) The method of claim 16, wherein all n reactive groups of the scaffold precursor are contacted with and can react with the same peripheral moiety precursor subset.

54. (*Amended*) The method of claim 16, further comprising the steps:

(e) [contracting] contacting a second biomolecule with the mass-coded combinatorial library, whereby members of the mass-coded combinatorial library which are ligands for the second biomolecule bind to the second biomolecule to form second biomolecule-ligand complexes;

(f) separating the second biomolecule-ligand complexes from the unbound members of the mass-coded combinatorial library;

(g) dissociating the second biomolecule-ligand complexes;

(h) determining the molecular mass of each ligand for the second biomolecule; and

(i) determining which molecular mass or masses determined in step (d) are not determined in step (h), thereby providing the molecular masses of members of the mass-coded combinatorial library which are ligands for the first biomolecule but are not ligands for the second biomolecule[.];

wherein each molecular mass determined in step (i) corresponds to a set of n peripheral moieties present in a ligand for the first biomolecule which is not a ligand for the second biomolecule, thereby identifying a member of the mass-coded combinatorial library which are ligands for the first biomolecule but are not ligands for the second biomolecule.

55. (*Amended*) The method of claim 54 wherein the first biomolecule and the second biomolecule are each, independently, a protein or a nucleic acid molecule.

56. (*Amended*) The method of claim 55 wherein the first biomolecule and the second biomolecule are each a protein, and the amino acid sequence of the second biomolecule is derived from the amino acid sequence of the first

biomolecule by insertion, deletion or substitution of one or more amino acid residues.

57. (*Amended*) The method of claim 55 wherein the first biomolecule is a first protein and the second biomolecule is a second protein, said first and second proteins having the same amino acid sequence, wherein said first and second proteins have different posttranslational modifications.

59. (*Amended*) The method of claim 55 wherein the second biomolecule is a complex of the first biomolecule with a ligand.

60. (*Amended*) The method of claim 55 wherein the first biomolecule and the second biomolecule are each immobilized on a solid support.

62. (*Amended*) The method of claim 55, wherein one or [more] both of steps (b) and (f) is performed by contacting a solution comprising first biomolecule-ligand complexes or second biomolecule-ligand complexes and unbound members of the mass-coded combinatorial library with a size exclusion chromatography column, whereby the unbound members of the mass-coded combinatorial library elute from the column after the first biomolecule-ligand complexes or the second biomolecule-ligand complexes.

63. (*Amended*) The method of claim 55, wherein one or both of steps (b) and (f) is performed by contacting a solution comprising first biomolecule-ligand complexes or second biomolecule-ligand complexes and unbound members of the mass-coded combinatorial library with a size exclusion [chromatography column] membrane, whereby the members of the mass-coded combinatorial library pass through said membrane and the first biomolecule-ligand complexes or second biomolecule-ligand complexes do not pass through said membrane.

~~64.~~ (*Amended*) A method for identifying a member of a mass-coded combinatorial library which is a ligand for a first biomolecule but is not a ligand for a second biomolecule, said mass-coded combinatorial library comprising compounds of the general formula $XY_n$, wherein n is an integer from 2 to about 6, X is a scaffold

[having n reactive groups], and each Y is, independently, a peripheral moiety, [wherein each reactive group is capable of reacting with at least one peripheral moiety precursor to form a covalent bond, and] wherein said mass-coded combinatorial library is produced by reacting a scaffold precursor having n reactive groups, wherein each reactive group is capable of reacting with at least one peripheral moiety precursor to form a covalent bond, with a peripheral moiety precursor subset selected from a peripheral moiety precursor set, said peripheral moiety precursor subset comprising a sufficient number of distinct peripheral moiety precursors such that there exist at least about 250 distinct combinations of n peripheral moieties derived from said peripheral moiety precursors, [wherein said subset includes at least two different peripheral moiety precursors that are each contacted with and can each react with at least two different reactive groups,] said method comprising the steps of:

(a) contacting the second biomolecule with the mass-coded combinatorial library, whereby members of the mass-coded combinatorial library which are ligands for the second biomolecule bind to the second biomolecule to form second biomolecule-ligand complexes and members of the mass-coded library which are not ligands for the second biomolecule remain unbound;

(b) separating the second biomolecule-ligand complexes from the unbound members of the mass-coded combinatorial library;

(c) contacting the first biomolecule with the unbound members of the mass-coded combinatorial library of step (b), whereby members of the mass-coded combinatorial library which are ligands for the first biomolecule bind to the first biomolecule to form first biomolecule-ligand complexes and members of the mass-coded library which are not ligands for the first biomolecule remain unbound;

(d) dissociating the first biomolecule-ligand complexes;

(e) determining the molecular mass of each ligand for the first biomolecule;

wherein each molecular mass determined in step (e) corresponds to a set of n peripheral moieties present in a ligand for the first biomolecule which is not a ligand for the second biomolecule, thereby identifying a member of the mass-coded combinatorial library which is a ligand for the first biomolecule but is not a ligand for the second biomolecule.

68. (*Amended*) A method for identifying a member of a mass-coded combinatorial library which is a first ligand for a biomolecule and binds the biomolecule at [the] a binding site of a known second ligand for the biomolecule, said mass-coded combinatorial library comprising compounds of the general formula $XY_n$, wherein [in] n is an integer from 2 to about 6, X is a scaffold [having n reactive groups], and each Y is, independently, a peripheral moiety, [wherein each reactive group is capable of reacting with at least one peripheral moiety precursor to form a covalent bond, and] wherein said mass-coded combinatorial library is produced by reacting a scaffold precursor having n reactive groups, wherein each reactive group is capable of reacting with at least one peripheral moiety precursor to forma covalent bond, with a peripheral moiety precursor subset selected from a peripheral moiety precursor set, said peripheral moiety precursor subset comprising a sufficient number of distinct peripheral moiety precursors such that there exists at least about 250 distinct combinations of n peripheral moieties derived from said peripheral moiety precursors, [wherein said subset includes at least two different peripheral moiety precursors that are each contacted with and can each react with at least two different reactive groups,] said method comprising the steps of:

a) contacting the biomolecule with the mass-coded combinatorial library, whereby members of the mass-coded combinatorial library which are ligands for the biomolecule bind to the biomolecule to form biomolecule-ligand complexes and members of the mass-coded combinatorial library which are not ligands for the biomolecule remain unbound;